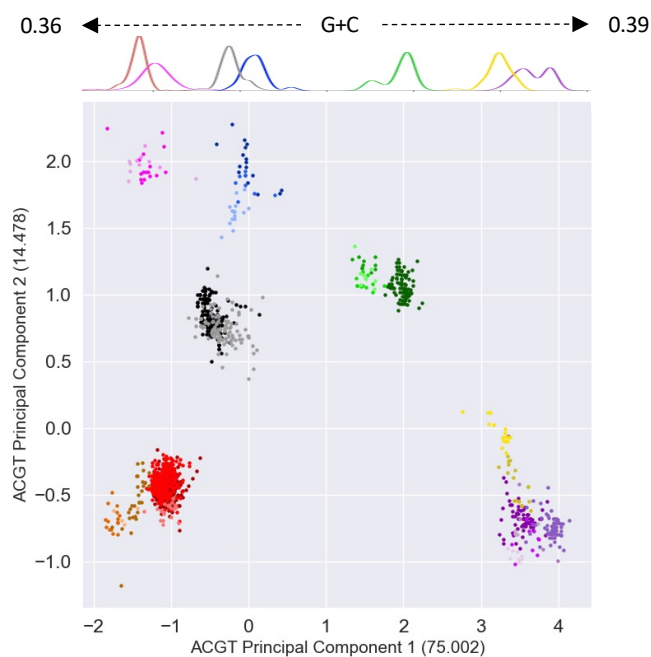


Base compositions from 1,278 complete *Alphapapillomavirus 9* genomes standardized to equal representation by HPV type superimposed on phylogenetic trajectories from the directional-drift (nhPhyML) estimate of the ancestral composition for the species.



G+C content superimposed on the first principal component of base compositions (see Figure 5) from 1,278 complete *Alphapapillomavirus 9* genomes.

